

FIG. 1

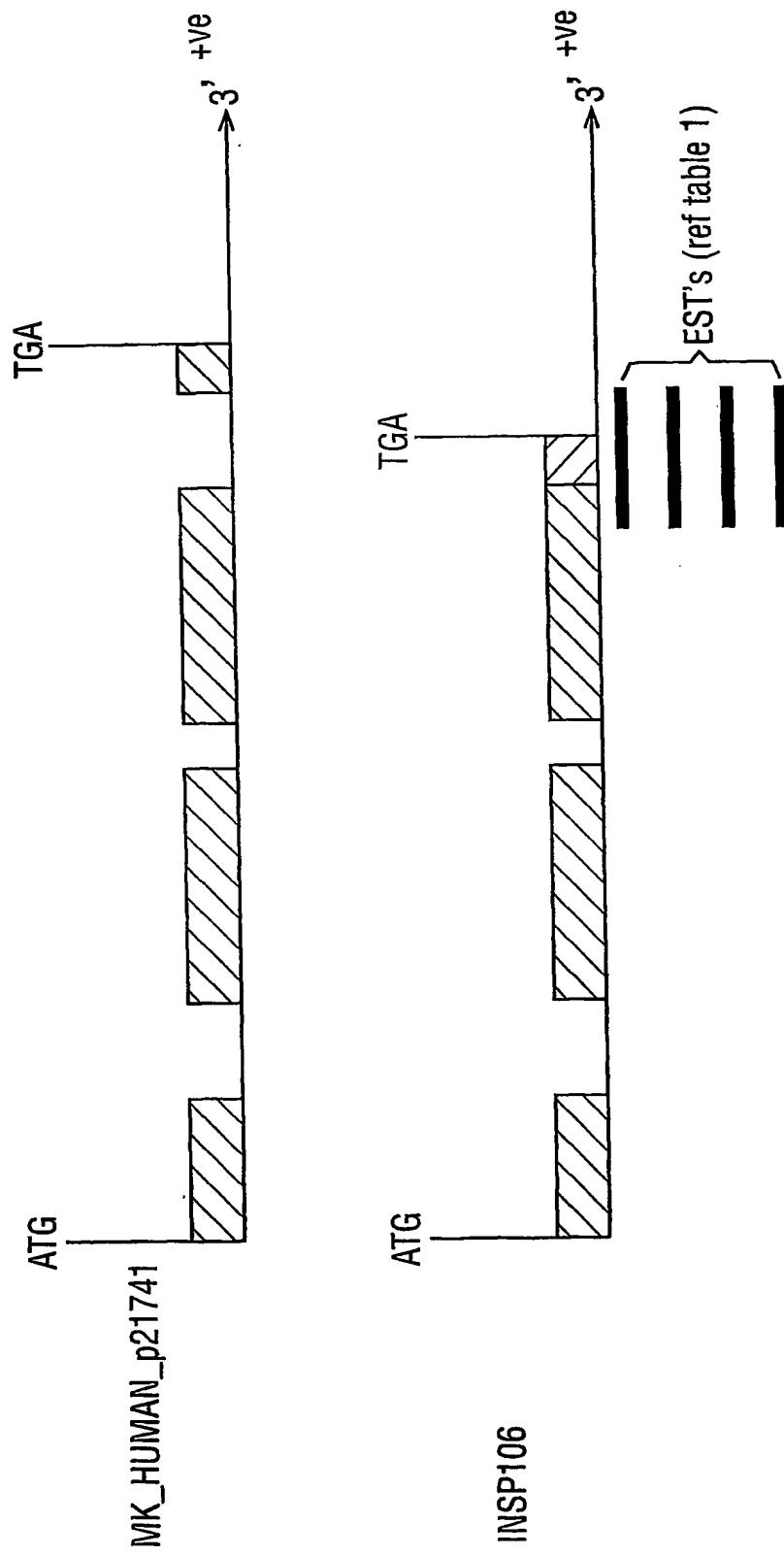
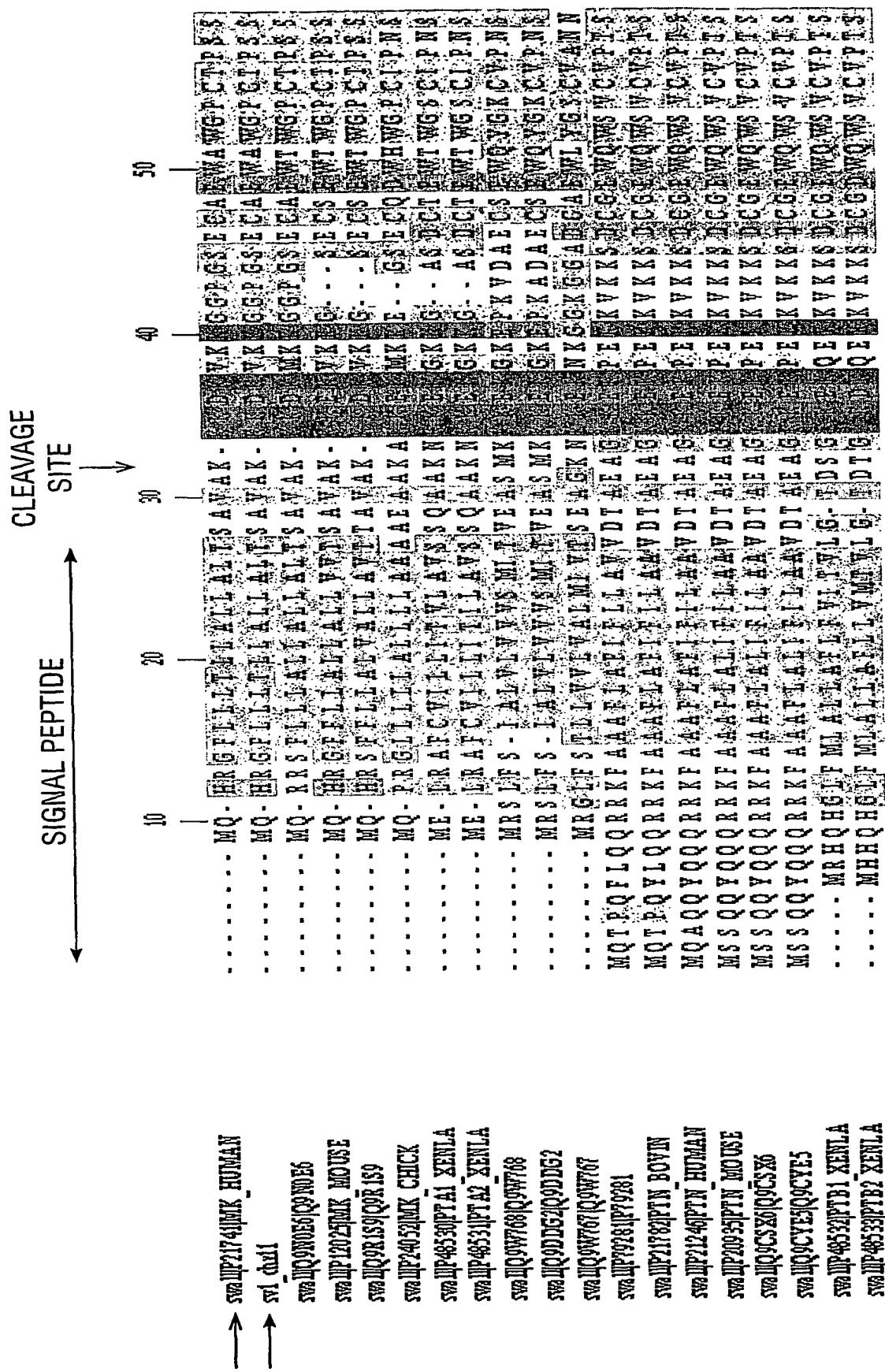
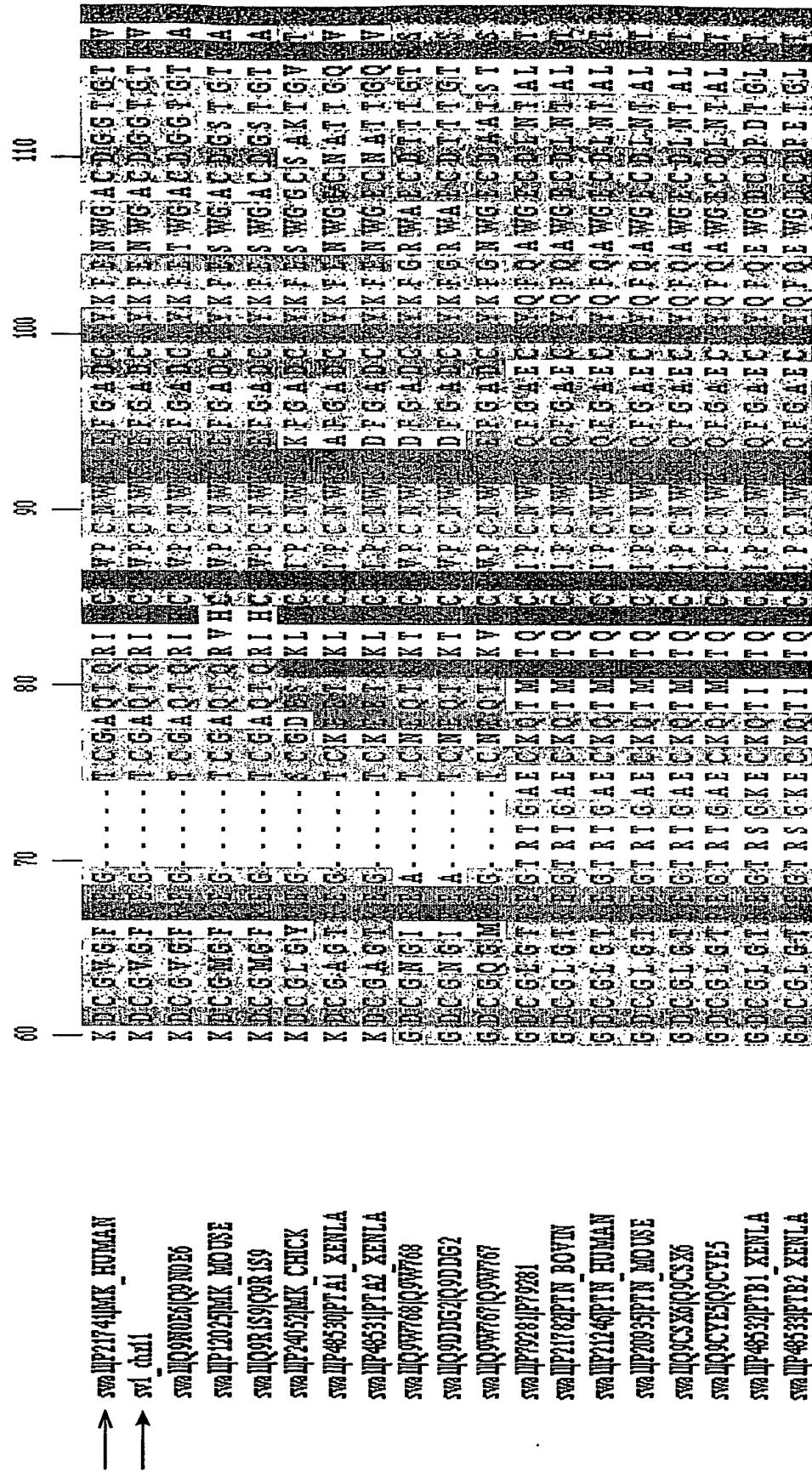


FIG. 2

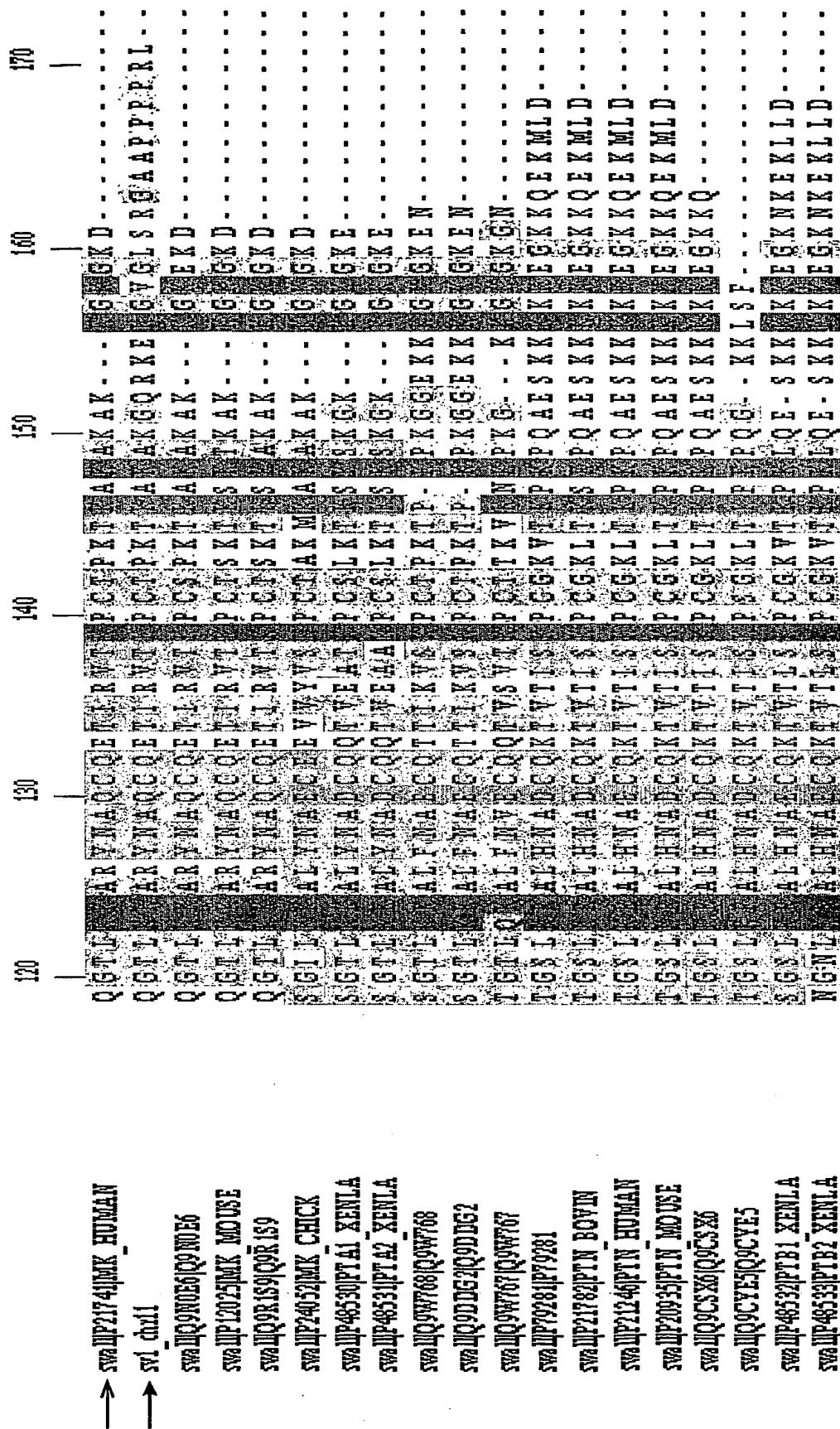


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FIG. 2 (CONT'D.)



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FIG. 3

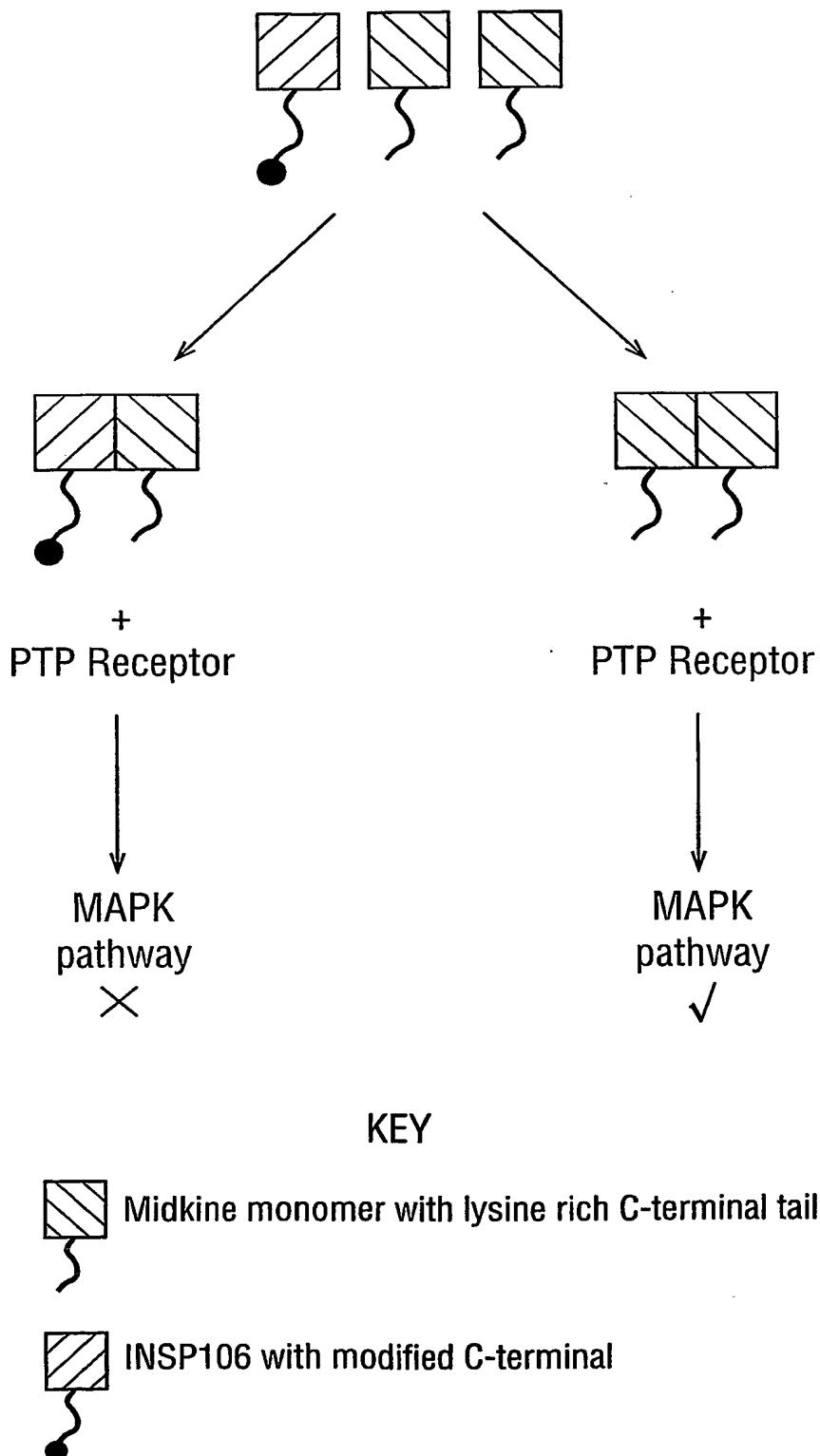


FIG. 4

10	20	30	40	50	60
swall MQHRGFLLTLALLTSAVAKKKDKVKKGPGSECAEWANGPCTPSSKDCGVGFREGT					
chr11_ MQHRGFLLTLALLTSAVAKKKDKVKKGPGSECAEWANGPCTPSSKDCGVGFREGT	10	20	30	40	50
70	80	90	100	110	120
swall CGAQTQRIRCRVPCNWKKKEFGADCKYKFENWGACDG GT GTKVVRQGTTLKKARYNAQCQETI					
chr11_ CGAQTQRIRCRVPCNWKKKEFGADCKYKFENWGACDG GT GTKVVRQGTTLKKARYNAQCQETI	70	80	90	100	110
130	140				
swall RVT K PCTPKTKAKAKA-KKGKG-----KD					
chr11_ RVT K PCTPKTKAKAKGQRKEKGVGLSRGAAPP PRL	130	140	150		

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FIG. 5

1 cggtgcgtcc gggctagcgg cgaggggccg cccaaagtct tcccacccgc gccacacctag
 61 cagccccact tggggcctgg aaagtggagc acgcggaggt gggagggccc tgcacgcggc
 121 ccccggtggg gaaggggacg ggccaggat tcagactcgg gctctccct caggatgcag
m q

181 caccgaggt tcctcctctt caccctcctc gccctgtgg cgctcacctc cgccgtcgcc
h r g f l l l t l l a l l a l t s a v a
INSP108-F1

241 aaaaagaaag ataaggtgaa gaagggcggc ccggggagcg agtgcgctga gtgggcctgg
k k k d k v k k g g p g s e c a e w a w

301 gggccctgca cccccagcag caaggattgc ggcgtgggtt tccgcgaggg cacctgcggg
g p c t p s s k d c g v g f r e g t c g

361 gcccagaccc agcgcatccg gtgcagggtg ccctgcaact ggaagaagga gtttggagcc
a q t q r i r c r v p c n w k k e f g a

421 gactgcaagt acaagtttga gaactgggt gcgtgtgatg gggcacagg caccaaagt
d c k y k f e n w g a c d g g t g t k v

481 cgccaaggca ccctgaagaa ggcgcgtac aatgctcagt gccaggagac catccgcgtc
r q g t l k k a r y n a q c q e t i r v

541 accaaggcct gcaccccaa gaccaaagca aaggccaaag gtcagcgaaa ggagaagggg
t k p c t p k t k a k a k g q r k e k g

601 gtggggctgt cgccccccgc tgccccccccc cccccccgc tgtgagggga caattccaag
v g l s r g a a p p p p r . l

661 ttAAACCTTA agtttgagt CCTGGCCAGT ggcttcctga catcgctca ctggcttcc
INSP108-R1

721 ctgcctggaa aagtctgaag atggcacta caagagagggc cgtaggtat gctggggaca
 781 taaatcctcc ctggccaaa tagggaccaa ctcaaactac tccattggag catctggctt
 841 aggac

Position and sense of PCR primers →
In italics: predicted signal peptide

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FIG. 6

1 caggatgcag caccgaggct tcctccctcaccctcgtgg cgctcaccc
 m q h r g f l l l t l l a l l a l t

INSP10R-F1

61 cgccgtcgcc aaaaagaaag ataaggtgaa gaagggcgcc ccggggagcg agtgcgctga
 s a v a k k k d k v k k g g p g s e c a

121 gtgggcctgg gggccctgca cccccagcag caaggattgc ggcgtgggtt tccgcgaggg
 e w a w g p c t p s s k d c g v g f r e

181 cacctgcggg gcccagaccc agcgcatccg gtgcagggtg ccctgcaact ggaagaagga
 g t c g a q t q r i r c r v p c n w k k

241 gtttggagcc gactgcaagt acaagttga gaactgggt gcgtgtgatg gggcacagg
 e f g a d c k y k f e n w g a c d g g t

301 caccaaagtc cgccaaggca ccctgaagaa ggcgctac aatgctcaatgctcaatgcccaggagac
 g t k v r q g t l k k a r y n a q c q e

361 catccgcgtc accaaggccct gcaccccaa gaccaaagca aaggccaaag gtcagcgaaa
 t i r v t k p c t p k t k a k a k g q r

421 ggagaagggg gtggggctgt cgccgggggc tgccccccccc cccccccgcctgtgagggga
 k e k g v g l s r g a a p p p p r l

481 caattccaag ttaaacctta agtttgagt cctggccagt ggcttcctga catcgctca
INSP10R-R1

541 cttggc

Position and sense of PCR primers →

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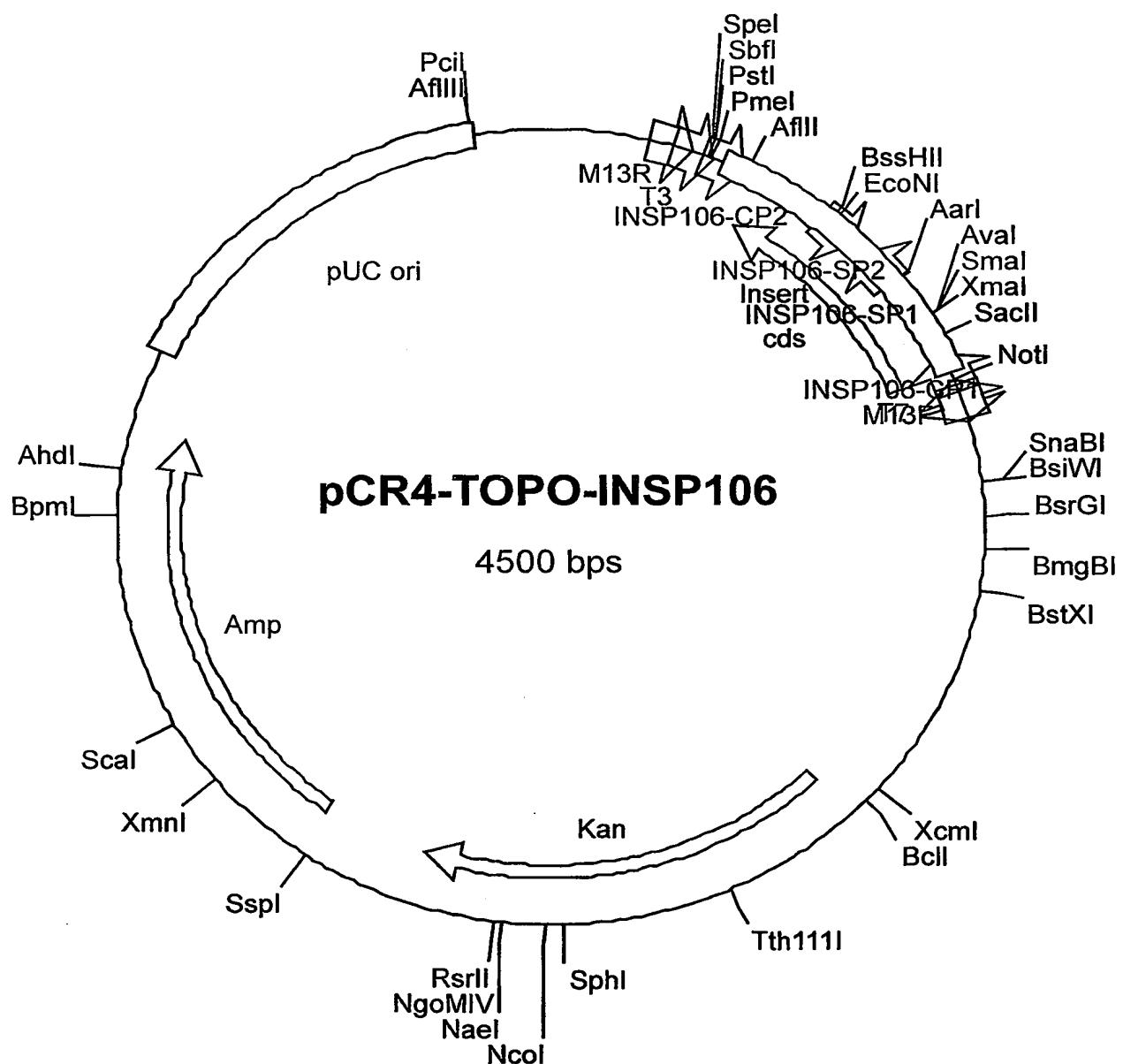
FIG. 7**Map of pCR4-TOPO-INSP106**

Molecule: pCR4-TOPO-INSP106, 4500 bps DNA Circular

Type	Start	End	Name	Description
MARKER	205		M13R	M13 rev priming site
MARKER	243		T3	T3 priming site
MARKER	295		INSP106-CP2	INSP106-CP2 primer site
MARKER	522		INSP106-SP2	INSP106-SP2 sequencing primer site
MARKER	616	C	INSP106-SP1	INSP106-SP1 sequencing primer site
GENE	833	366	C cds	INSP106 cds
MARKER	837	C	INSP106-CP1	INSP106-CP1 primer site
REGION	837	295	C Insert	INSP106-CP1/-CP2 PCR product
MARKER	890	C	T7	T7 priming site
MARKER	898		M13F	M13 for priming site
GENE	1702	2496	Kan	Kanamycin resistance gene ORF
GENE	2700	3560	Amp	Ampicillin resistance gene ORF
REGION	3705	4378	pUC ori	pUC origin

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FIG. 7(contd)



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FIG. 8

Map of pDONR 221

Molecule: pDONR221, 4759 bps DNA Circular
File Name: pDONR221.cm5

Description:

Type	Start	End	Name	Description
REGION	295	268	C rrnB T2	transcription termination sequence
REGION	470	427	C rrnB T1	transcription termination sequence
REGION	536	553	21M13	M13 Forward primer
REGION	570	801	attP1	
GENE	1197	1502	ccdB	
GENE	1844	2503	Cm r	Chloramphenicol resistance gene
REGION	2751	2982	attP2	
REGION	3040	3023	C M13 Rev	M13 Reverse primer
GENE	3153	3962	Kan r	
REGION	4083	4756	pUC ori	

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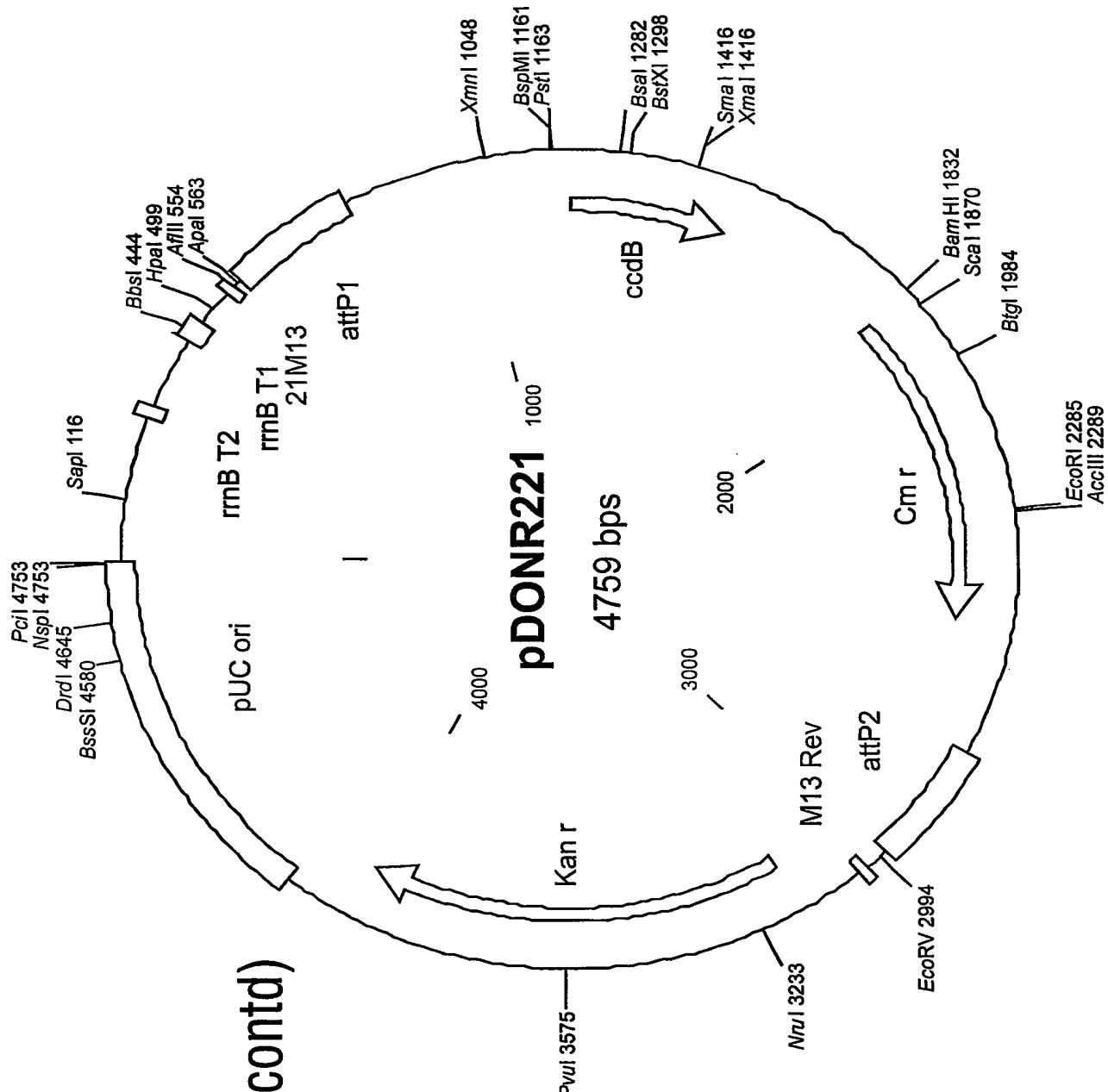


FIG. 8 (contd)

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FIG. 9

Map of expression vector pEAK12d

Molecule: pEAK12 d, 8760 bps DNA Circular
File Name: pEAK12DEST.cm5

Description: Mammalian cell expression vector (plasmid ID 11345)

Molecule Features:

Type	Start	End	Name	Description
REGION	2	595		pmb-ori
GENE	596	1519	Amp	
REGION	1690	2795	EF-1alpha	
REGION	2703	2722		position of pEAK12F primer
REGION	2796	2845		MCS
MARKER	2855		attR1	
GENE	3256	3915	CmR	
GENE	4257	4562	ccdB	
MARKER	4603		C attR2	
REGION	4733	4733		MCS
REGION	4734	5162		Poly A/splice
REGION	4819	4848	C	position of pEAK12R primer
GENE	5781	5163	C PUR	PUROMYCIN
REGION	6005	5782	C tK	tK promoter
REGION	6500	6006	C Ori P	
GENE	8552	6500	C EBNA-1	
REGION	8553	8752	sv40	

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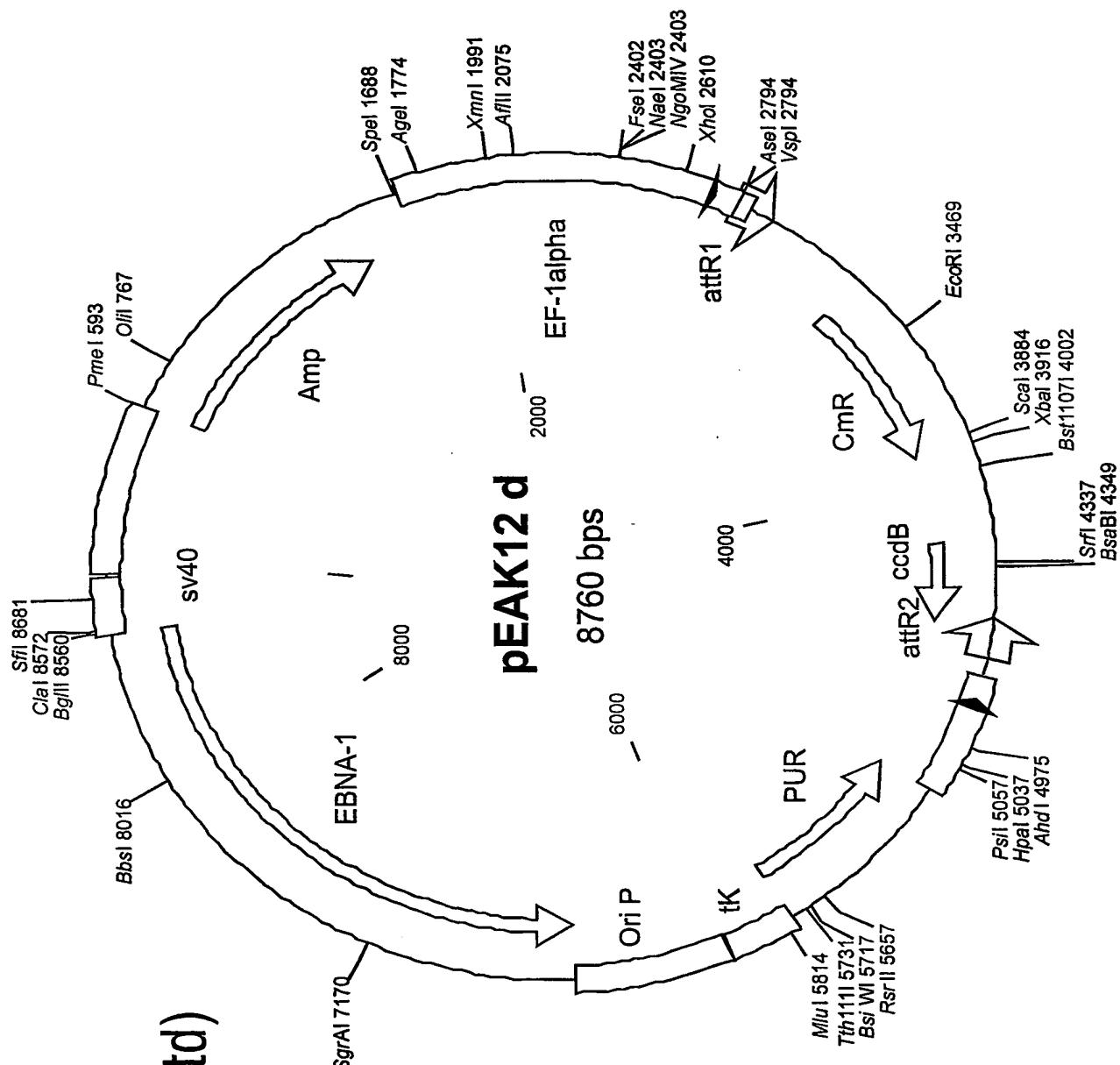


FIG. 9(contd)

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FIG. 10

Map of Expression vector pDEST12.2

Molecule: pDEST 12.2, 7278 bps DNA Circular
File Name: pDEST12-2.cm5

Description: Eukaryotic expression vector

Type	Start	End	Name	Description
REGION	15	608	CMV	CMV promoter
MARKER	648		M13R	M13R primer
REGION	687	706	SP6	SP6 promoter
REGION	730	854	attR1	
GENE	963	1622	Cm	
GENE	1964	2269	ccdB	
REGION	2310	2434	attR2	
GENE	2484	2464	C T7	T7 promoter
MARKER	2512		C 21M13	21M13 primer
REGION	2784	3050	pA	SV40 polyadenylation signal
REGION	3176	3631	f1	f1 intergenic region
REGION	3791	4099	P SV40	SV40 ori & early promoter
GENE	4158	4952	Neo	
REGION	5016	5064	pA	synthetic poly adenylation signal
GENE	5475	6335	Amp	
REGION	6480	7153	ori	pUC ori

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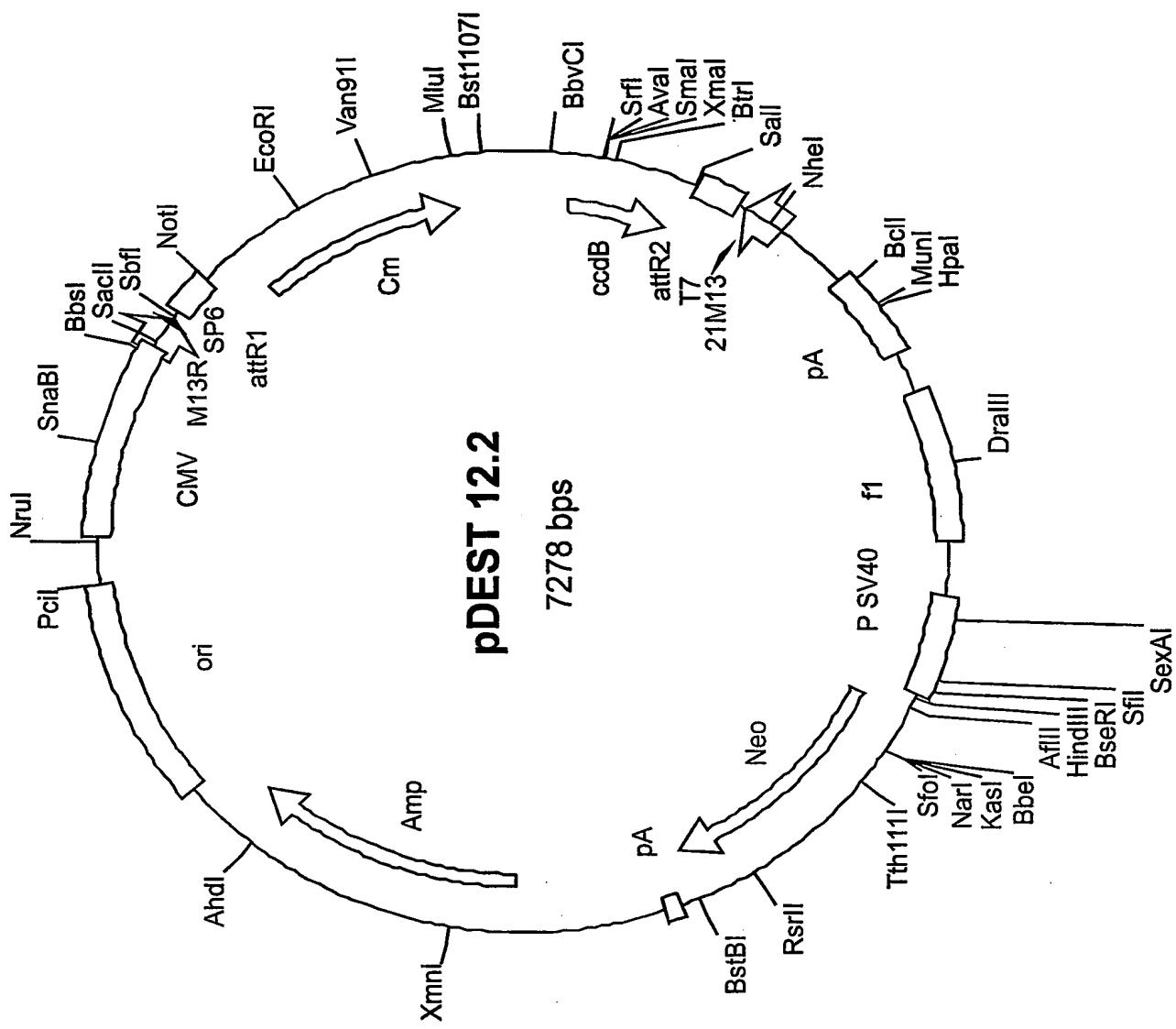


FIG. 10(contd)

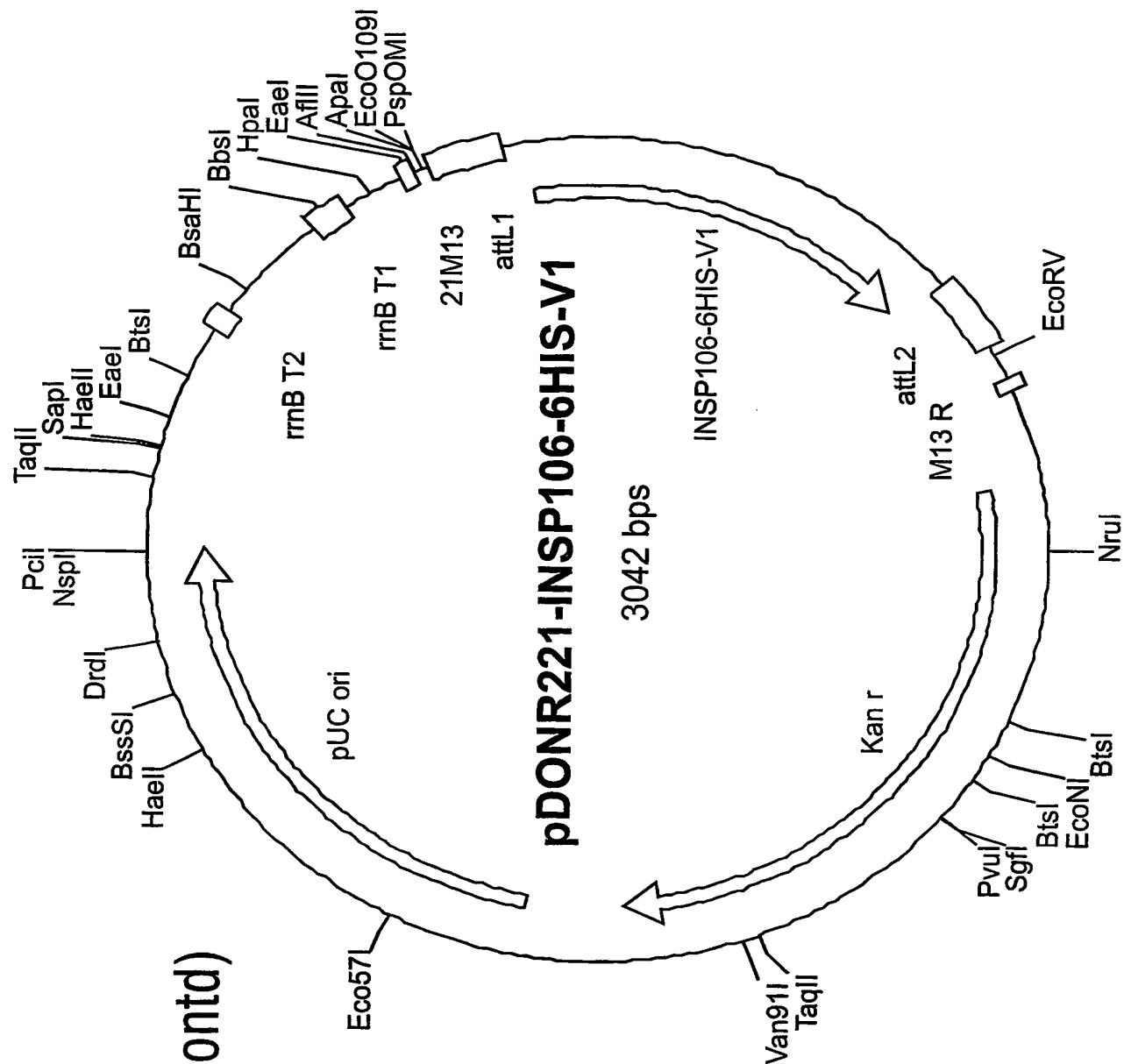
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FIG. 11

Map of pDONR221-INSPI06-6HIS

Molecule: pDONR221-INSPI06-6HIS-V1, 3042 bps DNA Circular

Type	Start	End	Name	Description
REGION	295	268	C rrnB T2	transcription termination sequence
REGION	470	427	C rrnB T1	transcription termination sequence
REGION	536	553	21M13	21M13 primer
REGION	570	651	attL1	
GENE	677	1162	INSPI06-6HIS-V1	
REGION	1177	1265	attL2	
REGION	1323	1307	C M13 R	M13R primer
GENE	1436	2245	Kan r	
GENE	2366	3039	pUC ori	



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FIG. 12

Map of pEAK12d-INSP106-6HIS

Molecule: pEAK12d-INSP106-6HIS-V1, 7435 bps DNA Circular

Type	Start	End	Name	Description
REGION	2	595	pmb-ori	
GENE	596	1519	Amp	
REGION	1690	2795	EF-1alpha	
REGION	2796	2845	MCS''	
REGION	2855	2874	attB1	
GENE	2888	3373	INSP106-6HIS-V1	
REGION	3381	3402	attB2	
REGION	3408	3408	'MCS	
REGION	3409	3837	'A	poly A/splice
GENE	4456	3838	C PUR	PUROMYCIN
REGION	4680	4457	C tK	tK promoter
REGION	5175	4681	C Ori P	
GENE	7227	5175	C EBNA-1	
REGION	7228	7427	sv40	

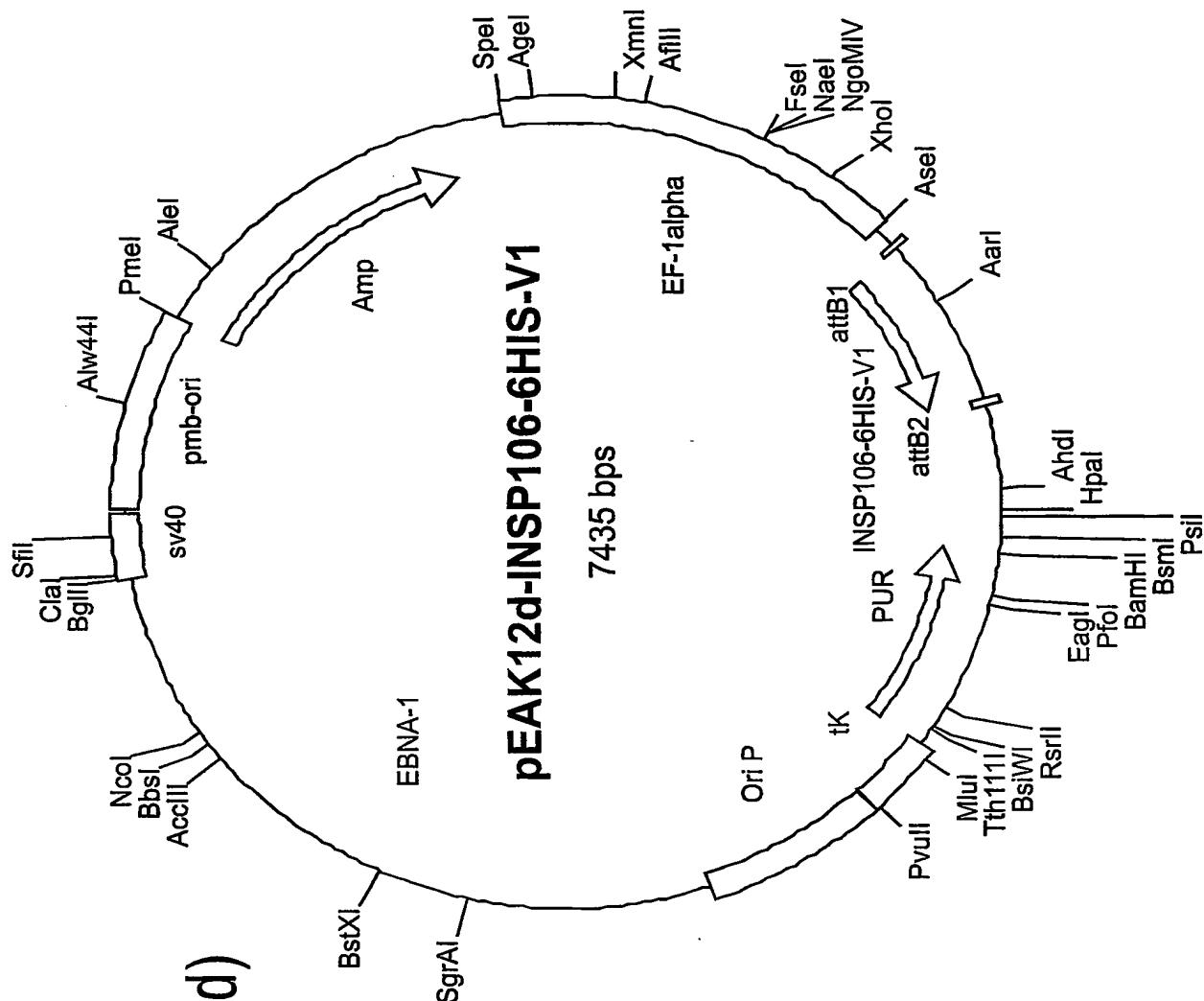


FIG. 12 (contd)

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FIG. 13

Map of pDEST12.2-INSP106-6HIS

Molecule: pDEST12.2-INSP106-6HIS-V1, 6121 bps DNA Circular

Type	Start	End	Name	Description
GENE	15	537	CMV promoter	
REGION	648	665	M13rev	M13R primer
REGION	687	704	SP6	SP6 primer
REGION	730	762	attB1	
GENE	763	1248	INSP106-6HIS-V1	
REGION	1252	1277	attB2	
REGION	1327	1307	C T7	T7 promoter
REGION	1356	1338	C 21M13	21M13 primer
GENE	1462	1824	pA	SV40 polyadenylation signal
GENE	2018	2474	f1	f1 intergenic region
GENE	2538	2956	P SV40	SV40 ori & early promoter
GENE	3001	3795	Neo	
GENE	3859	3907	pA	poly adenylation signal
GENE	4318	5178	Amp	
GENE	5327	5966	ori	pUC ori

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